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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of George E. Fox, Richard C. Willson III  
And Zhendong Zhang

**Serial No.: 10/057270**

Filed: January 26, 2002

For: ...Methods for the Determination of Genetic  
Affinity of Microorganisms and Viruses

Priority: Provisional 60/264,403 filed January 26, 2001

Attorney Docket: ..010AUS

Response Due: None yet

Examiner

Art Unit

**Invention Disclosure Statement**

37 CFR 1.501

Assistant Commissioner for Patents

Box US; Group 1743

Washington, DC 20231

Sir:

In respect to the enclosed USPTO Form 1447, the following remarks are intended to distinguish the references known to the inventors.

The undersigned Attorney certifies that this Document has been filed in the U.S. Post Office via Express Mail ET601010116US addressed as above to the USPTO on 9 March 2002 (37 CFR 1.10).

**The Invention**

This invention embodies selecting which sub-sequences in a database of nucleic acid such as 16S rRNA are highly characteristic of particular groupings of bacteria, microorganisms, fungi, etc. on a substantially phylogenetic tree. Also applicable to viruses comprising viral genomic RNA or DNA. A catalogue of highly characteristic sequences identified by this method is assembled to establish

the genetic affinity<sup>1</sup> of an unknown organism. The characteristic sequences are used to design nucleic acid hybridization probes that include the characteristic sequence or its complement, or are derived from one or more characteristic

35 sequences. A plurality of these characteristic sequences is used in hybridization to determine the phylogenetic tree position of the organism(s) in a sample. Those target organisms represented in the original sequence database and sufficient characteristic sequences can identify to the species or subspecies level.

Oligonucleotide arrays of many probes are especially preferred. A hybridization  
40 signal can comprise fluorescence, chemiluminescence, or isotopic labeling, etc.; or sequences in a sample can be detected by direct means, e.g. mass spectrometry.

The method's characteristic sequences can also be used to design specific PCR primers. The method uniquely identifies the phylogenetic affinity of an unknown organism without requiring prior knowledge of what is present in the sample. Even  
45 if the organism has not been previously encountered, the method still provides useful information about which phylogenetic tree bifurcation nodes encompass the organism.

## 50 The Prior Art

Prior Art will include the following References:

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<sup>1</sup> "Genetic affinity" refers to how closely related two organisms are on a substantially phylogenetic tree. An organism has the highest genetic affinity to the smallest (i.e. most peripheral) cluster that encompasses it. On a substantially phylogenetic tree that is represented by signature probes in the assay, the invention determines what grouping encompasses an organism(s) in the test sample.

1. Fox, GE, Pechman, KR, and Woese, CR (1977) *Comparative cataloging of 16S Ribosomal Ribonucleic Acid: Molecular Approach to Prokaryotic Systematics. Intn. J. Syst. Bacteriol.* 27:44-57 (1977).

This paper describes methodology by which a bifurcating tree based on genetic affinity can be obtained from oligonucleotide sub-sequences of a large RNA. The subsequences are generated by a method known as oligonucleotide cataloging in which all fragments of an RNA ending in G but containing no internal G's are generated experimentally and individually sequenced. The method of the current invention does not seek to obtain trees of genetic affinity. Rather it utilizes the information contained in such trees to identify individual signature oligonucleotides that can be used in hybridization assays to determine the genetic affinity of organisms or viruses that may be present in a test sample.

2. Fox GE, Stackebrandt E, Hespel RB, Gibson J, Maniloff J, Dyer TA, Wolfe RS, Balch WE, Tanner RS, Magrum LJ, Zablen LB, Blakemore R, Gupta R, Bonen L, Lewis BJ, Stahl DA, Luehrsen KR, Chen KN, and Woese CR (1980) *The phylogeny of prokaryotes. Science* 209:457-463.

This paper describes the outcome of studies of genetic affinity among known organisms using partial sequence data from 16S ribosomal RNA that is generated by a method known as oligonucleotide cataloging. It was the first comprehensive tree published that displayed actual genetic affinity between most major bacterial groupings. The method of the invention does not seek to obtain trees of genetic affinity. Rather it utilizes the information contained in such trees to identify signature oligonucleotides that can be used in assays to determine the genetic affinity of organisms or viruses that may be present in a test sample.

3. Kohne, David E.; *Method for detecting identifying and quantitating organisms and viruses*; US Patent 5,288,611 granted 22 Feb 1994 which claims:

85 "1. A method for detecting the presence of a species of organism comprising a ribosomal nucleic acid sequence, in a test sample, comprising the steps of: contacting ribosomal nucleic acid from said test sample with a nucleic acid probe able to hybridize to only a portion of said ribosomal nucleic acid sequence of said organism,  
90 incubating said probe and said ribosomal nucleic acid obtained from said test sample under specified."

This patent describes a method of using a nucleic acid probe targeted to ribosomal RNA in order to detect the presence of a specific targeted organism. The  
95 method of the invention seeks to determine the genetic affinity of whatever organism(s) is present in the test sample as closely as allowed by the probes included in the assay. When using the method of the present invention one need not know before hand which specific organisms might be present in the test sample and one can use target molecules other than ribosomal RNA. The method of the  
100 invention also provides a mechanism for identifying signature sequences that can be used to design suitable hybridization probes.

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4. Kohne, David E.; *Method for detection, identification and quantitation of non-viral organisms*; US Patent 4,851,330 granted 25 July 1989 which claims:

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115 "A method for detecting the presence in a test sample of any non-viral organisms belonging to a group, said group consisting of at least one but less than all non-viral organisms; which comprises: (a) bringing together any test sample rRNA and a nucleic acid probe, said probe having been selected to be sufficiently complementary to hybridize to one or more rRNA subunit subsequences that are specific to said group of non-viral organisms and to be shorter in length than the rRNA subunit to which said probe hybridizes; (b) incubating the probe and any test sample rRNA under specified hybridization conditions such that said probe hybridizes to the rRNA of said group of non-viral organisms and does not detectably hybridize to rRNA from other non-viral organisms; and, (c) assaying for hybridization of said probe to any test sample rRNA.

125 This patent describes a method of using a nucleic acid probe targeted to ribosomal RNA in order to detect the presence of a specific targeted group of organisms. The method of the 330 patent also utilizes a probe, which has been selected by differential hybridization. When using the method of the present invention one need not know before hand which specific group of organisms might be present in the test sample and one can use target molecules other than ribosomal RNA. Moreover, the method of the present invention seeks to determine genetic affinity not to detect a particular organism group. The method of the invention can be used with nucleic acids other than rRNA and also provides a mechanism for identifying signature sequences that can be used to design suitable hybridization probes.

135 5. Maidak BL, Cole JR, Lilburn TG, Parker CT Jr, Saxman PR, Stredwick JM, Garrity GM, Li B, Olsen GJ, Pramanik S, Schmidt TM, and Tiedje JM (2000) The RDP (Ribosomal Database Project) continues. *Nucleic Acids Res.* 28:173-174.

140 This paper describes a public database, which contains ribosomal RNA sequence information and bifurcating trees based on genetic affinity that can be calculated from that data. It also provides search tools that facilitate the design of hybridization probes that target specific organisms. This database is a very useful source of the type of information used to implement the method of the invention. It  
145 does not provide methods of identifying signature sequences needed to design signature probes and it does not describe methods for rapidly determining genetic affinity based on hybridization using signature probes.

150 6. McGill TR, Jurka J, Sobieski JM, Pickett MH, Woese CR, and Fox GE (1986) *Characteristic archaeobacterial 16S rRNA oligonucleotides. Syst. Appl. Microbiol.* 7:194-197.

This paper describes a means of identifying ribonuclease T<sub>1</sub> signature sequences in oligonucleotide catalog data sets (lists of sequence subsequences consisting only of  
155 fragments of a ribosomal RNA ending in G which containing no internal G's). The approach described provides a formal way to define the ribonuclease T<sub>1</sub> signature sequences needed for an alternative method of evaluate higher-order branching possibilities generated by the usual clustering methods and to find placements for organisms that are not well handled by the usual clustering methods. Unlike the  
160 present invention, the method of this paper is not envisioned as a means to design probes that could be used in a rapid assay for genetic affinity. The current invention identifies signature sequences from any RNA or DNA without any of the sequence restrictions that apply to ribonuclease T<sub>1</sub> oligonucleotides and envisions the use of the resulting information as the basis for the design of hybridization  
165 probes. These probes can be used to determine the genetic affinity of organisms or

viruses containing the target RNA or DNA in a sample without prior knowledge of what organism or virus is likely to be present.

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- ✓ 7. Uchida, T., Bonen, L., Schaup, HW, Lewis, BJ, Zablen, L., and Woese, C (1974) *The use of ribonuclease U<sub>2</sub> in RNA Sequence Determination. J. Molec. Evol.* 3:63-77.

175 This paper describes the experimental procedures and analysis methods used to obtain ribonuclease T<sub>1</sub> catalog data and specifically outlines the utility of using ribonuclease U<sub>2</sub> to accomplish this. The information in this paper is essential to understanding some of the other papers and patents that are referenced. Unlike the present invention, this paper does not describe methods for rapidly determining genetic affinity based on hybridization.

180

- ✓ 8. Woese CR (1987) *Bacterial evolution. Microbiol. Rev.* 51:221-271.

185 This review paper discusses in detail the genetic affinity of bacteria, and to limited extent eukaryotic organisms, as determined from 16S rRNA sequence and catalog data. It also introduces the idea of sequence signatures, which are "individual positions in the molecule, sequence signatures that define the various groupings". Examples of such individual signature positions that are highly characteristic of specific organisms groupings are given and used to evaluate the validity of the genetic affinities seen in phylogenetic trees constructed from 16S rRNA sequence data. The approach does not consider the quality of these individual position  
190 sequence signatures and it is not explained how one could obtain useful hybridization probes from just individual positions. Moreover, unlike the present

invention, this paper does not describe methods for rapidly determining genetic affinity based on hybridization.

195 9. Woese CR, Maniloff J, and Zablen LB (1980) *Phylogenetic analysis of the mycoplasmas. Proc. Natl. Acad. Sci. USA* 77:494-498.

This paper reports experimentally determined ribonuclease T<sub>1</sub> oligonucleotide catalog data for several organisms. The genetic affinity of these organisms is  
200 studied by a method called "signature analysis". According to this methodology "a set of oligonucleotides that is characteristic of (unique to) a group of organisms defines that group and is a "signature" for the group". This approach seeks to define genetic affinity of known organisms. The signature here is defined to be a collection of ribonuclease T<sub>1</sub> oligonucleotides that together define a group of  
205 organisms that have genetic affinity. The notion that a single oligonucleotide sequence could be used as a signature probe or to design signature probes is not considered. Unlike the present invention, the method of this paper is not envisioned as a means for rapidly determining the genetic affinity of an unknown organism. The current invention utilizes a substantially phylogenetic tree to identify  
210 individual signature oligonucleotides from any RNA or DNA without the sequence restrictions that apply to ribonuclease T<sub>1</sub> oligonucleotides and envisions the use of the resulting information as the basis for the design of hybridization probes that can be used to determine the genetic affinity of organisms or viruses containing the target RNA or DNA in a sample without prior knowledge of what organism or  
215 virus is likely to be present.



10. Woese CR, Stachebrandt E, Weisburg WG, Paster BJ, Madigan MT, Fowler VJ, Hahn CM, Blanz P, Gupta R, Nealson KH, and Fox GE (1984) *The phylogeny of purple bacteria: the alpha subdivision. System. Appl. Microbiol.* 5:315-326.

This paper applies the signature approach developed by Woese, Maniloff and Zablen (see above; Proc. Natl. Acad. Sci. USA 77:494-498)) to evaluate genetic affinities among various species of *Pseudomonas* deduced from ribonuclease T<sub>1</sub> oligonucleotide catalog data. The signature approach described by the authors is not envisioned as a method of designing hybridization probes or rapidly determining the genetic affinity of an unknown organism in a test sample. The current invention provides the means to identify individual signature oligonucleotides from any RNA or DNA without the sequence restrictions that apply to ribonuclease T<sub>1</sub> oligonucleotides and envisions the use of the resulting information as the basis for the design of hybridization probes that can be used to determine the genetic affinity of organisms or viruses containing the target RNA or DNA in a sample without prior knowledge of what organism or virus is likely to be present.

11. Woese; C. R., Stackebrandt, E., Macke, T. J., and Fox, G. E. "A Phylogenetic Definition of the Major Eubacterial Taxa", *System Appl. Microbiol.* 6: 143-151 (1985)

This paper describes methodology to display the distribution of any ribonuclease T<sub>1</sub> oligonucleotide in a database of approximately 400 16S rRNA catalogs. This made it easier for the user of the graphical display to subjectively identify the ribonuclease T<sub>1</sub> sequences that together formed the signature of a particular phylogenetic grouping. The method described does

245 not take advantage of a signature quality function and it is implemented for  
the purpose of defining genetic relationships among known organisms rather  
than identifying the genetic affinity of an unknown organism. The method of  
the current invention identifies signature sequences from any RNA or DNA  
without any sequence restriction and envisions the use of the resulting  
250 information as the basis for the design of hybridization probes.

### **Differences From Prior Art**

255 The invention uniquely and rapidly identifies the phylogenetic affinity of an  
unknown organism without requiring prior knowledge of what is present in the  
sample. The invention is determining genetic affinity rather than detecting or  
identifying. This is a major distinction from Kohnne and similar methods.

260 Woese's "sequence signature" method does not consider the quality of the  
individual position sequence signatures and it does not teach how one could obtain  
useful hybridization probes from these one base sequence signatures. Woese's  
earlier "signature analysis" (including the McGill *et al.* refinements) focuses  
exclusively on ribonuclease T<sub>1</sub> oligonucleotides which have substantial sequence  
265 restrictions. Moreover, the purpose of this method was to either evaluate the  
quality of phylogenetic trees produced by methods such as cluster analysis and/or  
to independent of such methods determine phylogenetic relationships. Unlike the  
present invention, Woese does not describe methods for rapidly determining  
genetic affinity based on hybridization. In contrast to Woese's method, the current  
270 invention does not seek to either make or evaluate a substantially phylogenetic

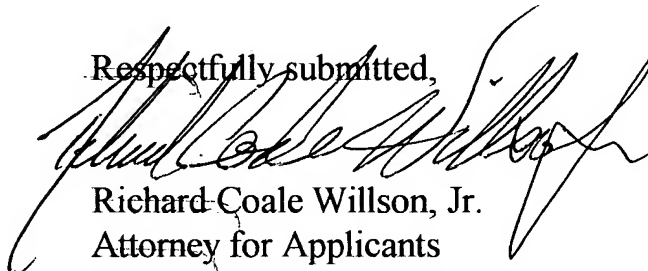
Rather, it uses the information on such a tree to determine signature sequences that will be useful in designing probes that can be used to rapidly determine genetic affinity.

275 There is a additional literature that we did not specifically cite because it is less relevant and relates to the use of RNA/RNA or RNA/DNA hybridization to determine genetic similarity between organisms. Such methods use whole rRNA as the probe or perhaps restriction fragments and certainly do not base their probes on an existing tree so they are less relevant to the present invention. Still other less  
280 relevant literature relates to direct sequencing or other methods of determining genetic affinity.

This invention offers several important improvements over the methods taught by the above prior art as it is understood:

- 285 A. Provides a method of rapidly determining the genetic affinity of previously ~~totally unknown~~ organisms.
- B. Can provide ~~information on the identities of~~ several organisms present in the same sample, even if none has been seen before.
- C. Can be based on non-RNA, even non-nucleic acid signatures, or mixed  
290 signatures using ~~information from nucleic acids~~, protein composition, phenotypic activities such as enzymatic activities.

Respectfully submitted,

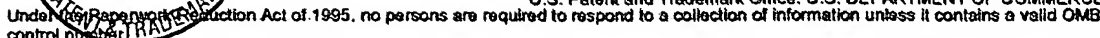
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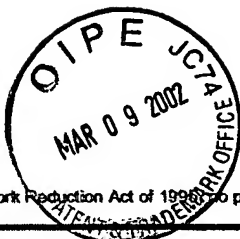
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<b>Substitute for form 1449B/PTO</b> <b>INFORMATION DISCLOSURE STATEMENT BY APPLICANT</b> (use as many sheets as necessary)		<b>Complete if Known</b>	
		Application Number	10/057270
		Filing Date	26 Jan 2002
		First Named Inventor	FOX
		Group Art Unit	
		Examiner Name	
Sheet <u>2</u> of <u>3</u>		Attorney Docket Number	D10AUS

OTHER PRIOR ART - NON PATENT LITERATURE DOCUMENTS			
Examiner Initials	Cite No. <sup>1</sup>	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published	T <sup>2</sup>
	1	FOX, Comparative cataloguing... Systemics INTN. J. Syst. Bacteriol. <u>27</u> , 44-57 (1977)	
	2	FOX, The phylogeny of prokaryotes Science <u>209</u> , 451-463 (1980)	
	5	MAIDAK, The RDP... continues Nucleic Acids Res. <u>28</u> , 173-174 (2000)	
	6	McGill et al, Characteristic... oligonucleotides Syst. Microbiol., <u>7</u> , 194-197 (1986)	
	7	UCHIDA et al, The use of... Determination J. Molec. Evol. <u>3</u> , 63-77 (1974)	
	8	WOESE, Bacterial evolution Microbiol. Rev. <u>51</u> , 221-271 (1987)	
	9	WOESE, Phylogenetic... mycoplasmas Proc. Natl Acad. Sci. <u>77</u> , 494-498	

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## INFORMATION DISCLOSURE STATEMENT BY APPLICANT

Sheet 1 of 3

Application Number	10/057,270
Filing Date	26 Jan, 2002
First Named Inventor	FOX
Group Art Unit	
Examiner Name	
Attorney Docket Number	A10A05

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